

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Rodier, Patricia M.
Ingram, Jennifer L.
Figlewicz, Denise A.
Hyman, Susan L.
Stodgell, Christopher J.
- (ii) TITLE OF INVENTION: GENETIC POLYMORPHISMS WHICH ARE
ASSOCIATED WITH AUTISM SPECTRUM DISORDERS
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
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(C) CITY: Rochester
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 14603-1051
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/049,803
(B) FILING DATE: 17-JUN-1997
- (viii) ATTORNEY/AGENT INFORMATION:
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(C) REFERENCE/DOCKET NUMBER: 176/60181
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1008 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGACAAATG CAAGAACATGAA CTCCTTCCTG GAATACCCCA TACTTAGCAG TGGCGACTCG 60
GGGACCTGCT CAGCCCGAGC CTACCCCCTCG GACCATAGGA TTACAACCTTT CCAGTCGTGC 120
GCGGTCAGCG CCAACAGTTG CGGCGGCGAC GACCAGCTTCC TAGTGGGCAG GGGGGTGCAG 180
ATCGGTTCGC CCCACCACCA CCACCACAC CACCACCAAC ACCCCCCAGCC GGCTACCTAC 240
CAGACTTCCG GGAACCTGGG GGTGTCTAC TCCCACCAA GTTGTGGTCC AAGCTATGGC 300
TCACAGAACT TCAGTGCGCC TTACAGCCCC TACCGTTAA ATCAGGAAGC AGACGTAAGT 360
GGTGGGTACC CCCAGTGCGC TCCCGCTGTT TACTCTGGAA ATCTCTCATC TCCCATGGTC 420
CAGCATCACC ACCACCACCA GGGTTATGCT GGGGGCGCGG TGGGCTCGCC TCAATACATT 480
CACCACTCAT ATGGACAGGA GCACCAGAGC CTGGCCCTGG CTACGTATAA TAACTCCTTG 540
TCCCCTCTCC ACGCCAGCCA CCAAGAAGCC TGTCGCTCCC CCGCATCGGA GACATCTTCT 600
CCAGCGCAGA CTTTGACTG GATGAAAGTC AAAAGAAACC CTCCCAAAAC AGGGAAAGTT 660
GGAGAGTACG GCTACCTGGG TCAACCCAAC GCGGTGCGCA CCAACTTCAC TACCAAGCAG 720
CTCACGGAAC TGGAGAAGGA GTTCCACTTC AACAAAGTACC TGACGCGCGC CCGCAGGGTG 780
GAGATCGCTG CATCCCTGCA GCTCAACGAG ACCCAAGTGA AGATCTGGTT CCAGAACCGC 840
CGAATGAAGC AAAAGAAACG TGAGAAGGAG GGTCTCTTGC CCATCTCTCC GGCCACCCCG 900
CCAGGAAACG ACGAGAAGGC CGAGGAATCC TCAGAGAAAGT CCAGCTCTTC GCCCTGCGTT 960
CCTTCCCCGG GGTCTTCTAC CTCAGACACT CTGACTACCT CCCACTGA 1008

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 335 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Asp	Asn	Ala	Arg	Met	Asn	Ser	Phe	Leu	Glu	Tyr	Pro	Ile	Leu	Ser
1						5			10				15		
Ser	Gly	Asp	Ser	Gly	Thr	Cys	Ser	Ala	Arg	Ala	Tyr	Pro	Ser	Asp	His
						20			25				30		
Arg	Ile	Thr	Thr	Phe	Gln	Ser	Cys	Ala	Val	Ser	Ala	Asn	Ser	Cys	Gly
						35			40			45			

Gly Asp Asp Arg Phe Leu Val Gly Arg Gly Val Gln Ile Gly Ser Pro
50 55 60

His His His His His His His His His Pro Gln Pro Ala Thr Tyr
65 70 75 80

Gln Thr Ser Gly Asn Leu Gly Val Ser Tyr Ser His Ser Ser Cys Gly
85 90 95

Pro Ser Tyr Gly Ser Gln Asn Phe Ser Ala Pro Tyr Ser Pro Tyr Ala
100 105 110

Leu Asn Gln Glu Ala Asp Val Ser Gly Gly Tyr Pro Gln Cys Ala Pro
115 120 125

Ala Val Tyr Ser Gly Asn Leu Ser Ser Pro Met Val Gln His His His
130 135 140

His His Gln Gly Tyr Ala Gly Gly Ala Val Gly Ser Pro Gln Tyr Ile
145 150 155 160

His His Ser Tyr Gly Gln Glu His Gln Ser Leu Ala Leu Ala Thr Tyr
165 170 175

Asn Asn Ser Leu Ser Pro Leu His Ala Ser His Gln Glu Ala Cys Arg
180 185 190

Ser Pro Ala Ser Glu Thr Ser Ser Pro Ala Gln Thr Phe Asp Trp Met
195 200 205

Lys Val Lys Arg Asn Pro Pro Lys Thr Gly Lys Val Gly Glu Tyr Gly
210 215 220

Tyr Leu Gly Gln Pro Asn Ala Val Arg Thr Asn Phe Thr Thr Lys Gln
225 230 235 240

Leu Thr Glu Leu Glu Lys Glu Phe His Phe Asn Lys Tyr Leu Thr Arg
245 250 255

Ala Arg Arg Val Glu Ile Ala Ala Ser Leu Gln Leu Asn Glu Thr Gln
260 265 270

Val Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Gln Lys Lys Arg Glu
275 280 285

Lys Glu Gly Leu Leu Pro Ile Ser Pro Ala Thr Pro Pro Gly Asn Asp
290 295 300

Glu Lys Ala Glu Glu Ser Ser Glu Lys Ser Ser Ser Ser Pro Cys Val
305 310 315 320

Pro Ser Pro Gly Ser Ser Thr Ser Asp Thr Leu Thr Thr Ser His
325 330 335

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1008 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGACAATG CAAGAACATGAA CTCCTTCCTG GAATACCCCA TACTTAGCAG TGGCGACTCG 60
GGGACCTGCT CAGCCCGAGC CTACCCCCTCG GACCATAGGA TTACAACCTTT CCAGTCGTGC 120
GCGGTCAGCG CCAACAGTTG CGGCGGCGAC GACCGCTTCC TAGTGGGCAG GGGGGTGCAG 180
ATCGGTTCGC CCCACCACCA CCACCACAC CACCATGCC ACCCCCCAGCC GGCTACCTAC 240
CAGACTTCCG GGAACCTGGG GGTGTCTAC TCCCACCAA GTTGTGGTCC AAGCTATGGC 300
TCACAGAACT TCAGTGCGCC TTACAGCCCC TACCGCTTAA ATCAGGAAGC AGACGTAAGT 360
GGTGGGTACC CCCAGTGCGC TCCCGCTGTT TACTCTGGAA ATCTCTCATC TCCCATGGTC 420
CAGCATCAC ACCACCACCA GGGTTATGCT GGGGGCGCGG TGGGCTCGCC TCAATAACATT 480
CACCACTCAT ATGGACAGGA GCACCAGAGC CTGGCCCTGG CTACGTATAA TAATCCTTG 540
TCCCCTCTCC ACGCCAGCCA CCAAGAAGCC TGTCGCTCCC CCGCATCGGA GACATCTTCT 600
CCAGCGCAGA CTTTGACTG GATGAAAGTC AAAAGAAACC CTCCCAAAAC AGGGAAAGTT 660
GGAGAGTACG GCTACCTGGG TCAACCCAAC GCGGTGCGCA CCAACTTCAC TACCAAGCAG 720
CTCACGGAAC TGGAGAAGGA GTTCCACTTC AACAAAGTACC TGACGCGCGC CCGCAGGGTG 780
GAGATCGCTG CATCCCTGCA GCTCAACGAG ACCCAAGTGA AGATCTGGTT CCAGAACCGC 840
CGAATGAAGC AAAAGAAACG TGAGAAGGAG GGTCTCTTGC CCATCTCTCC GGCCACCCCG 900
CCAGGAAACCG ACGAGAAGGC CGAGGAATCC TCAGAGAAGT CCAGCTCTTC GCCCTGCGTT 960
CCTTCCCCGG GGTCTTCTAC CTCAGACACT CTGACTACCT CCCACTGA 1008

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 335 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Asn Ala Arg Met Asn Ser Phe Leu Glu Tyr Pro Ile Leu Ser
1 5 10 15

Ser Gly Asp Ser Gly Thr Cys Ser Ala Arg Ala Tyr Pro Ser Asp His
20 25 30

Arg Ile Thr Thr Phe Gln Ser Cys Ala Val Ser Ala Asn Ser Cys Gly
35 40 45

Gly Asp Asp Arg Phe Leu Val Gly Arg Gly Val Gln Ile Gly Ser Pro
50 55 60

His His His His His His His Arg His Pro Gln Pro Ala Thr Tyr
65 70 75 80

Gln Thr Ser Gly Asn Leu Gly Val Ser Tyr Ser His Ser Ser Cys Gly
85 90 95

Pro Ser Tyr Gly Ser Gln Asn Phe Ser Ala Pro Tyr Ser Pro Tyr Ala
100 105 110

Leu Asn Gln Glu Ala Asp Val Ser Gly Gly Tyr Pro Gln Cys Ala Pro
115 120 125

Ala Val Tyr Ser Gly Asn Leu Ser Ser Pro Met Val Gln His His His
130 135 140

His His Gln Gly Tyr Ala Gly Gly Ala Val Gly Ser Pro Gln Tyr Ile
145 150 155 160

His His Ser Tyr Gly Gln Glu His Gln Ser Leu Ala Leu Ala Thr Tyr
165 170 175

Asn Asn Ser Leu Ser Pro Leu His Ala Ser His Gln Glu Ala Cys Arg
180 185 190

Ser Pro Ala Ser Glu Thr Ser Ser Pro Ala Gln Thr Phe Asp Trp Met
195 200 205

Lys Val Lys Arg Asn Pro Pro Lys Thr Gly Lys Val Gly Glu Tyr Gly
210 215 220

Tyr Leu Gly Gln Pro Asn Ala Val Arg Thr Asn Phe Thr Thr Lys Gln
225 230 235 240

Leu Thr Glu Leu Glu Lys Glu Phe His Phe Asn Lys Tyr Leu Thr Arg
245 250 255

Ala Arg Arg Val Glu Ile Ala Ala Ser Leu Gln Leu Asn Glu Thr Gln
260 265 270

Val Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Gln Lys Lys Arg Glu
275 280 285

Lys Glu Gly Leu Leu Pro Ile Ser Pro Ala Thr Pro Pro Gly Asn Asp
290 295 300

Glu Lys Ala Glu Glu Ser Ser Glu Lys Ser Ser Ser Ser Pro Cys Val
305 310 315 320

Pro Ser Pro Gly Ser Ser Thr Ser Asp Thr Leu Thr Thr Ser His
325 330 335

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1021 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGACGCATGG ACTATAATAG GATGAACTCC TTCTTAGAGT ACCCACTCTG TAACCAGGGGA 60
CCCAGCGCCT ACAGCGCCCA CAGCGCCCCA ACCTCCTTTC CCCCAAGCTC GGCTCAGGCG 120
GTTGACAGCT ATGCAAGCGA GGGCCGCTAC GGTGGGGGGC TGTCCAGCCC TGCGTTTCAG 180
CAGAACTCCG GCTATCCCGC CCAGCAGCCG CCTTCGACCC TGGGGGTGCC CTTCCCCAGC 240
TCCCGGCCCT CGGGGTATGC TCCTGCCGCC TGCAAGCCCA GCTACGGGCC TTCTCAGTAC 300
TACCCCTCTGG GTCAATCAGA AGGAGACGGA GGCTATTTC ATCCCTCGAG CTACGGGCC 360
CAGCTAGGGG GCTTGTCCGA TGGCTACGGA GCAGGGTGGAG CCGGTCCGGG GCCATATCCT 420
CCGCAGCATC CCCCTTATGG GAACGAGCAG ACCGCGAGCT TTGCACCGGC CTATGCTGAT 480
CTCCTCTCCG AGGACAAGGA AACACCCTGC CCTTCAGAAC CTAACACCCC CACGGCCCGG 540
ACCTTCGACT GGATGAAGGT TAAGAGAAC CCACCCAAGA CAGCGAAGGT GTCAGAGCCA 600
GGCCTGGCT CGCCCAGTGG CCTCCGCACC AACTCACCA CAAGGCAGCT GACAGAACTG 660
GAAAAGGAGT TCCATTCAA CAAGTACCTG AGCCGGGCC GGAGGGTGGA GATTGCCGCC 720
ACCCTGGAGC TCAATGAAAC ACAGGTCAAG ATTTGGTTCC AGAACCGACG AATGAAGCAG 780
AAGAAGCGCG AGCGAGAGGG AGGTCGGGTC CCCCCAGCCC CACCAGGCTG CCCCCAAGGAG 840
GCAGCTGGAG ATGCCTCAGA CCAGTCGACA TGCACCTCCC CGGAAGCCTC ACCCAGCTCT 900
GTCACCTCCT GAACTGAACC TAGCCACCAA TGGGGCTTCC AGGCACGTGGA GCGCCCCAGT 960
CCAGCCCTAT CCCAGGCTCT CCCAACCCAG GCCTGGCTTC ACTGCCTGGG ATCTCTAGGC 1020
T 1021

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Asp Tyr Asn Arg Met Asn Ser Phe Leu Glu Tyr Pro Leu Cys Asn
1 5 10 15

Arg Gly Pro Ser Ala Tyr Ser Ala His Ser Ala Pro Thr Ser Phe Pro
20 25 30

Pro Ser Ser Ala Gln Ala Val Asp Ser Tyr Ala Ser Glu Gly Arg Tyr
35 40 45

Gly Gly Gly Leu Ser Ser Pro Ala Phe Gln Gln Asn Ser Gly Tyr Pro
50 55 60

Ala Gln Gln Pro Pro Ser Thr Leu Gly Val Pro Phe Pro Ser Ser Ala
65 70 75 80

Pro Ser Gly Tyr Ala Pro Ala Ala Cys Ser Pro Ser Tyr Gly Pro Ser
85 90 95

Gln Tyr Tyr Pro Leu Gly Gln Ser Glu Gly Asp Gly Gly Tyr Phe His
100 105 110

Pro Ser Ser Tyr Gly Ala Gln Leu Gly Gly Leu Ser Asp Gly Tyr Gly
115 120 125

Ala Gly Gly Ala Gly Pro Gly Pro Tyr Pro Pro Gln His Pro Pro Tyr
130 135 140

Gly Asn Glu Gln Thr Ala Ser Phe Ala Pro Ala Tyr Ala Asp Leu Leu
145 150 155 160

Ser Glu Asp Lys Glu Thr Pro Cys Pro Ser Glu Pro Asn Thr Pro Thr
165 170 175

Ala Arg Thr Phe Asp Trp Met Lys Val Lys Arg Asn Pro Pro Lys Thr
180 185 190

Ala Lys Val Ser Glu Pro Gly Leu Gly Ser Pro Ser Gly Leu Arg Thr
195 200 205

Asn Phe Thr Thr Arg Gln Leu Thr Glu Leu Glu Lys Glu Phe His Phe
210 215 220

Asn Lys Tyr Leu Ser Arg Ala Arg Arg Val Glu Ile Ala Ala Thr Leu
225 230 235 240

Glu Leu Asn Glu Thr Gln Val Lys Ile Trp Phe Gln Asn Arg Arg Met
245 250 255

Lys Gln Lys Lys Arg Glu Arg Glu Gly Gly Arg Val Pro Pro Ala Pro
260 265 270
Pro Gly Cys Pro Lys Glu Ala Ala Gly Asp Ala Ser Asp Gln Ser Thr
275 280 285
Cys Thr Ser Pro Glu Ala Ser Pro Ser Ser Val Thr Ser
290 295 300

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1030 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGACGCATGG ACTATAATAG GATGAACTCC TTCTTAGAGT ACCCACTCTG TAACCAGGGGA 60
CCCAGCGCCT ACAGCGCCCA CAGCGCCCCAC AGCGCCCCAA CCTCCTTTCC CCCAAGCTCG 120
GCTCAGGCAGG TTGACAGCTA TGCAAGCGAG GGCGCTACG GTGGGGGGCT GTCCAGGCCCT 180
GCGTTTCAGC AGAACTCCGG CTATCCGCC CAGCAGCCGC CTTCGACCCCT GGGGGTGCCC 240
TTCCCCAGCT CCGCGCCCTC GGGGTATGCT CCTGCCGCCT GCAGCCCCAG CTACGGGCCT 300
TCTCAGTACT ACCCTCTGGG TCAATCAGAA GGAGACGGAG GCTATTTCA TCCCTCGAGC 360
TACGGGGCCC AGCTAGGGGG CTTGTCCGAT GGCTACGGAG CAGGTGGAGC CGGTCCGGGG 420
CCATATCCTC CGCAGCATCC CCCTTATGGG AACGAGCAGA CCGCGAGCTT TGCACCGGCC 480
TATGCTGATC TCCTCTCCGA GGACAAGGAA ACACCCCTGCC CTTCAGAACCC TAACACCCCC 540
ACGGCCCGGA CCTTCGACTG GATGAAGGTT AAGAGAAACC CACCCAAGAC AGCGAAGGTG 600
TCAGAGCCAG GCCTGGGCTC GCCCAGTGGC CTCCGCACCA ACTTCACCAC AAGGCAGCTG 660
ACAGAACTGG AAAAGGAGTT CCATTCAAC AAGTACCTGA GCCGGGCCCG GAGGGTGGAG 720
ATTGCCGCCA CCCTGGAGCT CAATGAAACA CAGGTCAAGA TTTGGTTCCA GAACCGACGA 780
ATGAAGCAGA AGAAGCGCGA GCGAGAGGGA GGTCGGGTCC CCCCAGCCCC ACCAGGCTGC 840
CCCAAGGAGG CAGCTGGAGA TGCCTCAGAC CAGTCGACAT GCACCTCCCC GGAAGCCTCA 900
CCCAGCTCTG TCACCTCCTG AACTGAACCT AGCCACCAAT GGGGCTTCCA GGCACCTGGAG 960
CGCCCCAGTC CAGCCCTATC CCAGGCTCTC CCAACCCAGG CCTGGCTTCA CTGCCTGGGA 1020
TCTCTAGGCT 1030

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asp Tyr Asn Arg Met Asn Ser Phe Leu Glu Tyr Pro Leu Cys Asn
1 5 10 15

Arg Gly Pro Ser Ala Tyr Ser Ala His Ser Ala His Ser Ala Pro Thr
20 25 30

Ser Phe Pro Pro Ser Ser Ala Gln Ala Val Asp Ser Tyr Ala Ser Glu
35 40 45

Gly Arg Tyr Gly Gly Leu Ser Ser Pro Ala Phe Gln Gln Asn Ser
50 55 60

Gly Tyr Pro Ala Gln Gln Pro Pro Ser Thr Leu Gly Val Pro Phe Pro
65 70 75 80

Ser Ser Ala Pro Ser Gly Tyr Ala Pro Ala Ala Cys Ser Pro Ser Tyr
85 90 95

Gly Pro Ser Gln Tyr Tyr Pro Leu Gly Gln Ser Glu Gly Asp Gly Gly
100 105 110

Tyr Phe His Pro Ser Ser Tyr Gly Ala Gln Leu Gly Gly Leu Ser Asp
115 120 125

Gly Tyr Gly Ala Gly Gly Ala Gly Pro Gly Pro Tyr Pro Pro Gln His
130 135 140

Pro Pro Tyr Gly Asn Glu Gln Thr Ala Ser Phe Ala Pro Ala Tyr Ala
145 150 155 160

Asp Leu Leu Ser Glu Asp Lys Glu Thr Pro Cys Pro Ser Glu Pro Asn
165 170 175

Thr Pro Thr Ala Arg Thr Phe Asp Trp Met Lys Val Lys Arg Asn Pro
180 185 190

Pro Lys Thr Ala Lys Val Ser Glu Pro Gly Leu Gly Ser Pro Ser Gly
195 200 205

Leu Arg Thr Asn Phe Thr Thr Arg Gln Leu Thr Glu Leu Glu Lys Glu
210 215 220

Phe His Phe Asn Lys Tyr Leu Ser Arg Ala Arg Arg Val Glu Ile Ala
225 230 235 240

Ala Thr Leu Glu Leu Asn Glu Thr Gln Val Lys Ile Trp Phe Gln Asn
245 250 255

Arg Arg Met Lys Gln Lys Lys Arg Glu Arg Gly Gly Arg Val Pro
260 265 270

Pro Ala Pro Pro Gly Cys Pro Lys Glu Ala Ala Gly Asp Ala Ser Asp
275 280 285

Gln Ser Thr Cys Thr Ser Pro Glu Ala Ser Pro Ser Ser Val Thr Ser
290 295 300

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCATGGACTA TAATAGGATG

20

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TCTTGGGTGG GTTTCTCTTA

20